

EXHIBIT A: MARKED VERSION OF AMENDED CLAIMS
U.S. APPLICATION SERIAL NO. 09/616,849
(ATTORNEY DOCKET NO. 9301-044)

(as amended December 26, 2002)

27. (Three Times Amended) A method for evaluating a binding property of a polynucleotide probe comprising a predetermined nucleotide sequence to a target nucleotide sequence, said method comprising [comparing] determining a ratio of the amount of hybridization of polynucleotides in a first sample to the polynucleotide probe [with] and the amount of hybridization of polynucleotides in a second sample to the polynucleotide probe, wherein:

- (a) the first sample comprises a plurality of polynucleotide molecules comprising said target nucleotide sequence; and
- (b) the second sample comprises a plurality of different polynucleotide molecules wherein each different polynucleotide molecule comprises a sequence that is different from the nucleotide sequences of any other polynucleotide molecules in said plurality of different polynucleotide molecules,

wherein at least 75% of the polynucleotide molecules in said first sample are polynucleotide molecules comprising said target nucleotide sequence, and wherein said ratio is used as a measure of said binding property, thereby evaluating said binding property of said polynucleotide probe.

48. (Twice Amended) The method of claim 43 wherein [the amount of] each said polynucleotide molecule that does not comprise the target nucleotide sequence in the first sample is present in the second sample in an amount that differs from the amount of [the corresponding] said polynucleotide molecule in the [plurality of different polynucleotide molecules of the second] first sample by no more than a factor of 100.

49. (Twice Amended) The method of claim 43 wherein [the amount of] each said polynucleotide molecule that does not comprise the target nucleotide sequence in the first sample is present in the second sample in an amount that differs from the amount of [the corresponding] said polynucleotide molecule in the [plurality of different polynucleotide

molecules of the second] first sample by no more than a factor of 10.

50. (Twice Amended) The method of claim 43 wherein [the amount of] each said polynucleotide molecule that does not comprise the target nucleotide sequence in the first sample is present in the second sample in an amount that differs from the amount of [the corresponding] said polynucleotide molecule in the [plurality of different polynucleotide molecules of the second] first sample by no more than 50%.

51. (Twice Amended) The method of claim 43 wherein the mean abundance of the polynucleotide molecules that do not comprise the target nucleotide sequence in the first sample differs from the mean abundance of the different polynucleotide molecules that do not comprise the target nucleotide sequence in the plurality of different polynucleotide molecules of the second sample by no more than a factor of two.

52. (Twice Amended) The method of claim 43 wherein the mean abundance of the polynucleotide molecules that do not comprise the target nucleotide sequence in the first sample differs from the mean abundance of the different polynucleotide molecules that do not comprise the target nucleotide sequence in the plurality of different polynucleotide molecules of the second sample by no more than 50%.

53. (Twice Amended) The method of claim 43 wherein the mean abundance of the polynucleotide molecules that do not comprise the target nucleotide sequence in the first sample differs from the mean abundance of the different polynucleotide molecules that do not comprise the target nucleotide sequence in the plurality of different polynucleotide molecules of the second sample by no more than 10%.

54. (Twice Amended) The method of claim 43 wherein the mean abundance of the polynucleotide molecules that do not comprise the target nucleotide sequence in the first sample differs from the mean abundance of the different polynucleotide molecules that do not comprise the target nucleotide sequence in the plurality of different polynucleotide molecules of the second sample by no more than 1%.

Claims 57 and 58 have been canceled.

67. (Three Times Amended) A method for evaluating a binding property of a plurality of polynucleotide probes to a target nucleotide sequence wherein each polynucleotide probe in the plurality of polynucleotide probes comprises a predetermined nucleotide sequence, said method comprising [comparing] determining a ratio of the amount of hybridization of polynucleotides in a first sample to each polynucleotide probe in the plurality of polynucleotide probes [with] and the amount of hybridization of polynucleotides in a second sample to each polynucleotide probe in the plurality of polynucleotide probes, wherein:

- (a) the first sample comprises a plurality of polynucleotide molecules comprising said target nucleotide sequence; and
- (b) the second sample comprises a plurality of different polynucleotide molecules wherein each different polynucleotide molecule comprises a nucleotide sequence that is different from nucleotide sequence of any other polynucleotide molecules in said plurality of different polynucleotide molecules,

wherein at least 75% of the polynucleotide molecules in said first sample are polynucleotide molecules comprising said target nucleotide sequence, and wherein said ratio is used as a measure of said binding property, thereby evaluating said binding property of each said polynucleotide probe.

Claims 71 and 72 have been canceled.

75. (Twice Amended) The method of claim 67 wherein the first sample comprises two or more different polynucleotide molecules wherein none of the [plurality of] two or more different polynucleotide molecules hybridizes or cross-hybridizes to a probe that also hybridizes or cross-hybridizes to another one of the [plurality of] two or more different polynucleotide molecules.

90. (Amended) The method of any one of claims 27-30, 33-40, 42-54, 61-68, [71-75]

73-75 and 84-85, wherein said polynucleotide molecules comprising said target nucleotide sequence are the same polynucleotide molecule.